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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: FLECKENSTEIN, Bernhard
ALBRECHT, Jens-Christian
NEIPEL, Frank
FRIEDMAN-KIEN, Alvin
HUANG, Yao-Qi

(ii) TITLE OF INVENTION: VIRAL INTERLEUKIN-6

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: FOLEY & LARDNER
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(D) STATE: D.C.
(E) COUNTRY: U.S.A.
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/230,048
(B) FILING DATE: 12-MAR-1999
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO PCT/EP96/03199
(B) FILING DATE: 19-JUL-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Granados, Patricia D.
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(C) REFERENCE/DOCKET NUMBER: 058315/0129

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 672-5300
(B) TELEFAX: (202) 672-5399

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 612 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG TGC TGG TTC AAG TTG TGG TCT CTC TTG CTG GTC GGT TCA CTG CTG Met Cys Trp Phe Lys Leu Trp Ser Leu Leu Val Gly Ser Leu Leu	48
1 5 10 15	
GTA TCT GGA ACG CGG GGC AAG TTG CCG GAC GCC CCC GAG TTT GAA AAG Val Ser Gly Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe Glu Lys	96
20 25 30	
GAT CTT CTC ATT CAG AGA CTC AAT TGG ATG CTA TGG GTG ATC GAT GAA Asp Leu Leu Ile Gln Arg Leu Asn Trp Met Leu Trp Val Ile Asp Glu	144
35 40 45	
TGC TTC CGC GAC CTC TGT TAC CGT ACC GGC ATC TGC AAG GGT ATT CTA Cys Phe Arg Asp Leu Cys Tyr Arg Thr Gly Ile Cys Lys Gly Ile Leu	192
50 55 60	
GAG CCC GCT GCT ATT TTT CAT CTG AAA CTA CCA GCC ATC AAC GAT ACT Glu Pro Ala Ala Ile Phe His Leu Lys Leu Pro Ala Ile Asn Asp Thr	240
65 70 75 80	
GAT CAC TGC GGG TTA ATA GGA TTT AAT GAG ACT AGC TGC CTT AAA AAG Asp His Cys Gly Leu Ile Gly Phe Asn Glu Thr Ser Cys Leu Lys Lys	288
85 90 95	
CTC GCC GAT GGC TTT TTT GAA TTC GAG GTG TTG TTT AAG TTT TTA ACG Leu Ala Asp Gly Phe Phe Glu Phe Val Leu Phe Lys Phe Leu Thr	336
100 105 110	
ACG GAG TTT GGA AAA TCA GTG ATA AAC GTG GAC GTC ATG GAG CTT CTG Thr Glu Phe Gly Lys Ser Val Ile Asn Val Asp Val Met Glu Leu Leu	384
115 120 125	
ACG AAG ACC TTA GGA TGG GAC ATA CAG GAA GAG CTC AAT AAG CTG ACT Thr Lys Thr Leu Gly Trp Asp Ile Gln Glu Glu Leu Asn Lys Leu Thr	432
130 135 140	
AAG ACG CAC TAC AGT CCA CCC AAA TTT GAC CGC GGT CTA TTA GGG AGG Lys Thr His Tyr Ser Pro Pro Lys Phe Asp Arg Gly Leu Leu Gly Arg	480
145 150 155 160	
CTT CAG GGA CTT AAG TAT TGG GTG AGA CAC TTT GCT TCG TTT TAT GTT Leu Gln Gly Leu Lys Tyr Trp Val Arg His Phe Ala Ser Phe Tyr Val	528
165 170 175	
CTG AGT GCA ATG GAA AAG TTT GCA GGT CAA GCG GTG CGT GTT TTG GAC Leu Ser Ala Met Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp	576
180 185 190	
TCT ATC CCA GAC GTG ACT CCT GAC GTC CAC GAT AAG Ser Ile Pro Asp Val Thr Pro Asp Val His Asp Lys	612
195 200	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Cys Trp Phe Lys Leu Trp Ser Leu Leu Leu Val Gly Ser Leu Leu
1 5 10 15

Val Ser Gly Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe Glu Lys
20 25 30

Asp Leu Leu Ile Gln Arg Leu Asn Trp Met Leu Trp Val Ile Asp Glu
35 40 45

Cys Phe Arg Asp Leu Cys Tyr Arg Thr Gly Ile Cys Lys Gly Ile Leu
50 55 60

Glu Pro Ala Ala Ile Phe His Leu Lys Leu Pro Ala Ile Asn Asp Thr
65 70 75 80

Asp His Cys Gly Leu Ile Gly Phe Asn Glu Thr Ser Cys Leu Lys Lys
85 90 95

Leu Ala Asp Gly Phe Phe Glu Phe Glu Val Leu Phe Lys Phe Leu Thr
100 105 110

Thr Glu Phe Gly Lys Ser Val Ile Asn Val Asp Val Met Glu Leu Leu
115 120 125

Thr Lys Thr Leu Gly Trp Asp Ile Gln Glu Glu Leu Asn Lys Leu Thr
130 135 140

Lys Thr His Tyr Ser Pro Pro Lys Phe Asp Arg Gly Leu Leu Gly Arg
145 150 155 160

Leu Gln Gly Leu Lys Tyr Trp Val Arg His Phe Ala Ser Phe Tyr Val
165 170 175

Leu Ser Ala Met Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp
180 185 190

Ser Ile Pro Asp Val Thr Pro Asp Val His Asp Lys
195 200

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu
1 5 10 15

Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro Val Pro Pro
20 25 30

Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr
35 40 45

Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile
 50 55 60
 Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser
 65 70 75 80
 Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala
 85 90 95
 Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu
 100 105 110
 Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr
 115 120 125
 Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln
 130 135 140
 Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn
 145 150 155 160
 Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu
 165 170 175
 Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His
 180 185 190
 Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala
 195 200 205
 Leu Arg Gln Met
 210

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 211 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Phe Leu Ser Ala Arg Asp Phe His Pro Val Ala Phe Leu Gly
 1 5 10 15
 Leu Met Leu Val Thr Thr Ala Phe Pro Thr Ser Gln Val Arg Arg
 20 25 30
 Gly Asp Phe Thr Glu Asp Thr Thr Pro Asn Arg Pro Val Tyr Thr Thr
 35 40 45
 Ser Gln Val Gly Gly Leu Ile Thr His Val Leu Trp Glu Ile Val Glu
 50 55 60
 Met Arg Lys Glu Leu Cys Asn Gly Asn Ser Asp Cys Met Asn Asn Asp
 65 70 75 80

Asp Ala Leu Ala Glu Asn Asn Leu Lys Leu Pro Glu Ile Gln Arg Asn
85 90 95

Asp Gly Cys Tyr Gln Thr Gly Tyr Asn Gln Glu Ile Cys Leu Leu Lys
100 105 110

Ile Ser Ser Gly Leu Leu Glu Tyr His Ser Tyr Leu Glu Tyr Met Lys
115 120 125

Asn Asn Leu Lys Asp Asn Lys Lys Asp Lys Ala Arg Val Leu Gln Arg
130 135 140

Asp Thr Glu Thr Leu Ile His Ile Phe Asn Gln Glu Val Lys Asp Leu
145 150 155 160

His Lys Ile Val Leu Pro Thr Pro Ile Ser Asn Ala Leu Leu Thr Asp
165 170 175

Lys Leu Glu Ser Gln Lys Glu Trp Leu Arg Thr Lys Thr Ile Gln Phe
180 185 190

Ile Leu Lys Ser Leu Glu Glu Phe Leu Lys Val Thr Leu Arg Ser Thr
195 200 205

Arg Gln Thr
210